

Pred. No. is the number of results predicted by chance to have a

SOLVENTS

RESULTS
AC959795
CCDS
25,902 bp
AC959799
HOMO SAPIENS CHROMOSOME 17, CLONE HFX 62 F 16, CONTIGUA SUBCLONE
1994-11-24-OUT-1994

REFERENCE
1 (bases 1 to 154902)
AUTHORS
Birren, B., Linton, L., Nussbaum, C. and Landel, E.
TITLE
Homo sapiens chromosome 17, clone HREF, 62 p. 19
JOURNAL
Unpublished

REFERENCES
AUTHORS

2 (bases 1 to 154922)

Baker, B., Linton, L., Nustanu, C., Lander, E., Allen, N., Anderson, M., Barker, J., Baldwin, J., Barua, N., Becker, Y., Benayahu, S., Boutwell, C., Brown, A., Castle, A., Cerny, J., Cezuguelo, M., Collins, S., Collamore, A., Cooke, P., Corliss, D., Depierre, H., Denek, K., Dewar, K., Donnelly, S., Ferreira, P., FitzHugh, W., Forrest, C., Fudke, R., Gage, J., Gargyala, S., Garguery, K., Grant, G., Hayes, B., Heaford, A., Hendon, E., Horton, L., Howland, J., Jancot, B., Jones, C., Kann, L., Karakas, A., Lebecky, J., Macdonald, P., Marcus, N., McKean, P., McKusik, A., McKernan, K., Medline, M., McLean, M., Morris, W., Mychalek, J., Nair, P., Naylor, J., Nisfield, K., O'Connor, J., O'Connell, P., Pavlin, B., Peterson, K., Riley, K., Roberts, L., Roy, A., Sowers, P., Stange-Thomann, N., Stillwell, S., Stjepanovic, N., Stone, G., Subramanian, A., Tashfay, S., Tichetolsky, N., Terabea-Keller, J., Vassiliev, H., Vo, A., Wagner, A., Wheeler, M., Wu, Y., Wyman, C., Ye, W. J., Zhao, J. and Zody, M.

[illegible]


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Query Match      67.6%  Score 46.37  E-21  Length 237623
Best Local Similarity 88.6%  Pred. No. 6.5e-06
Matches 62: Conservative 0; Mismatches 7; Indels 1; Gaps 1;

27 1 CAGTGAATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 59
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28 121152 CAGTGAATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 121093

29 60 CCAAGATTAAG 69
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30 121192 CCAAGATTAAG 121083

RESULT 11
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LOCUS      519 bp  mRNA  linear  MAR 02-06-2001
DEFINITION  Oryctolagus cuniculus cAMP-dependent protein kinase subunit B1
ACCESSION  AF049893
VERSION     AF049893.1  GI:6602551
KEYWORDS   Oryctolagus cuniculus.
SOURCE      Oryctolagus cuniculus.
ORGANISM   Oryctolagus cuniculus.
REFERENCE  1 (bases 1 to 519)
AUTHORS   Qian, Z., Hao, C.M., Salter, K., Redha, P., and Breyer, M.D.
TITLE     Type II cAMP-dependent protein kinase regulates electrophoretic
JOURNAL   Am. J. Physiol. 276 (4 Pt 2): F622-F628 (1996)
MEDLINE   99216184
PUBMED    89198423
REFERENCE  2 (bases 1 to 519)
AUTHORS   Hao, C.M. and Breyer, M.D.
TITLE     Direct Submission
JOURNAL   Submitted (03-SEP-1998) Nephrology, Vanderbilt University, S-5223
MCN, Nashville, TN 37232, USA

FEATURES             source
     location/Qualifiers
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27 1 CAGTGAATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 59
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29 60 CCAAGATTAAG 69
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30 121192 CCAAGATTAAG 121083

Query Match      67.2%  Score 46.4;  E5.4;  Length 519;
Best Local Similarity 82.7%  Pred. No. 6.5e-06;
Matches 61: Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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28 121152 ATGCAATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 121093

29 61 CCAAGATTAAG 68
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30 121192 CCAAGATTAAG 121083

Query Match      67.2%  Score 46.4;  E5.4;  Length 519;
Best Local Similarity 82.7%  Pred. No. 6.5e-06;
Matches 61: Conservative 0; Mismatches 6; Indels 1; Gaps 1;

27 2 ATGCAATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 59
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28 121152 ATGCAATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 121093

29 61 CCAAGATTAAG 68
      ||||| |||||
30 121192 CCAAGATTAAG 121083

Query Match      67.2%  Score 46.4;  E5.4;  Length 519;
Best Local Similarity 82.7%  Pred. No. 6.5e-06;
Matches 61: Conservative 0; Mismatches 6; Indels 1; Gaps 1;

27 2 ATGCAATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 59
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28 121152 ATGCAATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 121093

29 61 CCAAGATTAAG 68
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30 121192 CCAAGATTAAG 121083

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KEYWORDS   Oryctolagus cuniculus.
SOURCE      Oryctolagus cuniculus.
ORGANISM   Oryctolagus cuniculus.
REFERENCE  1 (bases 1 to 445)
AUTHORS   Machuga, M.W. and Crowell, S.D.
TITLE     Estimate of the mutation rate for nucleotide in humans
JOURNAL   Genetics 150 (1): 297-304 (1990)
MEDLINE   20435744
PUBMED    20478242
REFERENCE  2 (bases 1 to 445)
AUTHORS   Machuga, M.W. and Crowell, S.D.
TITLE     Direct Submission
JOURNAL   Submitted (12-07-1999) Ecology and Evolutionary Biology,
University of Arizona, Bioresources West Building, Tucson, AZ 85721,
USA

FEATURES             source
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Query Match      61.2%  Score 46.4;  E5.4;  Length 260;
Best Local Similarity 73.7%  Pred. No. 6.7e-06;
Matches 41: Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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28 126 AGTCAGATTTTGGAGGCAATGCTTTCGCTCTCTTATCCGAGAGAGATGCTATTTCA 125

29 61 CCAAGATTAAG 68
      ||||| |||||
30 246 CCAAGATTAAG 253

RESULT 12
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LOCUS      445 bp  tRNA  linear  EFC 01-SEP-2000
DEFINITION  Pan troglodytes cAMP-dependent protein kinase regulatory subunit B1
alpha pseudogene, partial sequence.
VERSION     AF197635.1  GI:7012168
KEYWORDS   Pan troglodytes.
SOURCE      Pan troglodytes.
ORGANISM   Pan troglodytes.
REFERENCE  1 (bases 1 to 445)
AUTHORS   Machuga, M.W. and Crowell, S.D.
TITLE     Estimate of the mutation rate for nucleotide in humans
JOURNAL   Genetics 150 (1): 297-304 (1990)
MEDLINE   20435744
PUBMED    20478242
REFERENCE  2 (bases 1 to 445)
AUTHORS   Machuga, M.W. and Crowell, S.D.
TITLE     Direct Submission
JOURNAL   Submitted (12-07-1999) Ecology and Evolutionary Biology,
University of Arizona, Bioresources West Building, Tucson, AZ 85721,
USA

FEATURES             source
     location/Qualifiers
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     alpha"
     /note="B1 alpha"

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/db_xref="LOCUSID:67476"
/translation="MASGSMNLSDEESLHPTLYVCKHNIQALKKQSLVGLATTHH
RPMALREYPERLEKEEAKQICLOKTDIFIDSEDEISPPPTNPNVVKRRFGALSA
FVYTEEASYSVEKVLPKDYKIMAAIAKAEKVIYFSLLENERSTFLDAFPVSTIA
GETVIGGGEGENFYVIOGEMCVVKNEMAI SVGGSSGEGEALFYCTHAAIVKAK
TNVVLGIIIDPSYRRIMGSTLKKKKVEEPFSKVSILESLKKWRLIVATALEPVCF
EDGKIVVQEPGCEFFIILECTAAVALGRSENEFEVSGIAPSPSEALIMARP
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BASE COUNT      827 a      686 c      817 g      583 t
ORIGIN
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Query Match      62.6% Score 43.7; EH 10; Length 3313;
Best Local Similarity 86.8%; Pred. No. 2,001;
Matches 59; Conservative 0; Mismatches 8; Indels 2; Gaps 1;
QY      2 ASIGATATTTTGNSSCATGTTTTCGGTCTCCTTTATCCGAGAGACGTC-TATTCAS 60
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB     541 AGTGACATTTTGTATGATGATGTTTCAGATCTCCTTTATTCGAGAGACGTTATTCAS 60
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
CY      61 CAAGGTAA 66
      1 1 1 1 1 1
DB     602 CAAGGTGA 608
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